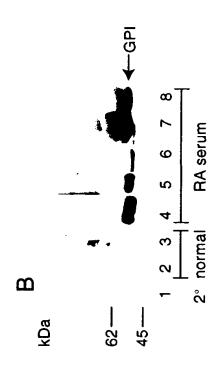


Fig. 1A



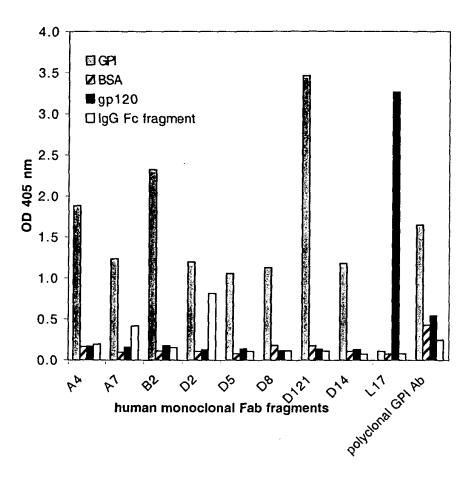


Fig. 2

## the and the train the state of the train to the train th

### FIG. 3AL Light Chain Variable AA Sequences

	PPKLLIY APKLLIY APRLLIY	PPKLLIY	APRLLIY	APRLLIY	APRLLIY	FR4	FGQGTKLEIKRTVA FGGGAKVGIRRTVA FGQGTKVEIKRTVA	FGQGTKLEIKRTVA	FGQGTRLEIKRTVA	FGQGTRLEIKRTVA	FGQGTKVEIKRTVA
FR2	WYQQKPGQPPKLLIY WYQLKPGKAPKLLIY WYQQKPGQAPRLLIY	WYQQKPGQPPKLLIY	WYQQRPGQAPRLLIY	WYQQKPGQAPRLLIY	WYQQKPGQAPRLLIY	CDR3	QQYYDSYT QQLNSYPLT QQYGSSPRT	QQYYDSYT	QQYDNVPDT	QQYGTSPL	QQYGSSPRT
CDR1	KSSQSVFYTSNNKNYLA RASQGISSYLA RASQSVSSSYLA	KSSQSVFYTSNNKNYLA	RASQSVSSSYLA	RASQSVSSSYLA	RASQSVSSSYLA		GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC GVPSRFSGSGSGTEFTLTISSLQPEDFATYYC GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	FTISSLQPEDTGTYYC	LTISRLEPEDFAVYYC	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC
FR1	PDSLAVSLGERATINC PSFLSASVGDRVTITC PGTLSLSPGERATLSC	PDSLAVSLGERATINC	PGTLSLSPGEGATLSC	PGTLSLSPGEGATLSC	PGTLSLSPGERVTLSC	FR3		GVPDRFSGSGSGTDF1	GIPDRFSGSGSGTDFSFTISSLQPEDTGTYYC	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	GIPDRFSGSGSGTDFT
SEQ ID NO:	1 2 3	4 F	5 F	9	7 I	CDR2	WASTRES AASTLQS GASSRAT	WASTRES	GASSRAT	GASSRAT	GASSRAT
Name	A4 D2 D121	B2	D14	D5	A7	Name cont'd	A4 D2 D121	B2	D14	DS	A7

### FIG. 3AH Heavy Chain Variable AA Sequences

	JKG	FQD /KG	S S	<sup>7</sup> QG	VH gene	VH3 VH3 VH3	VH1 VH3	VH4	VH1
	FYIESV Y.AD	SLAQSE FYADSV	YNRVFC	nyaqke	Þ	555			
CDR2	LLSSDGSNKFYIESVKG TM. VI.YNK.Y.AD	RINPTGGGVSLAQSFQD RISGNSGSTFYADSVKG	RIYGRGTTNYNRVFGS	GIIPPFGPVNYAQKFQG		MGQGTLVTVSS	VTVSS VTVSS	VNVFS	SSALA
	LLSSD TM. VI.Y.	RINE	RIYO	GIIE	FR4	WGQGTLVTVSS	WGQGTVVTVSS WGQGTTVTVSS	WGQGIVVNVFS	WGKGTTVTVSS
	4γ ∴ :	MG VS	IG	MG					SYMD
	WVRQAPGKGLEWVA 	WVRQAPGQGLQWMG WVRQAPGKGLEWVS	WVRQPVGKGLEWIG	WVRQAPGQGLEWMG			۶		VAYDGSGYYNNIPKIYYYSYMD V
FR2	WRQAP(	WRQAP WRQAP	WRQPV	VVRQAP	<b>8</b> 3	FNY . D .	EPLDL YYYGMD	YFDP	YYNNIP
					CDR3	SLVGTTAFNY .EAD.	PRFNMIREPLDL DLSSGAYYYYGMDV	DKGSEYSYFDP	AYDGSG
CDR1	SHGSH TM.	GHHIH SYAMN	GDSYFWS	RYAIS		SI.	P. IO	Ω	Λ Λ
	S · ·	L N	IK	ន		YCAI TN	FCAR YCAK	YCAR	YCAR
	SLKLSCAASGFTFS .LRV	SVRISCRASGNTFT	GPGLVRPSQTLSLTCPVSPGSIK	GAEVKKPGSSVKVSCRASGGTFS		RFTISKDNSKNTLYLQMNSLRIDDTAVYYCAI RLSPETN	RVSLTRDRSSNTVFLELSGLTEEDTALYFCAR RFTISRDNSKNTAFLRMNSQRAEDTAVYYCAK	RVSMSVDMSRSQFFLELRDVTAADTAVYYCAR	RVTITADDSTNTAYMGLSSLRSGDTAVYYCAR
FR1	LKLSCA LRV .R	VRISCF LRLSCP	LSLTCE	VKVSCF		INSLRII SPI	SGLTE! INSQRAI	RDVTA	SSLRS
	GGVVQPGRS	KPGTS /QPGGS	RPSQT	KRPGSS	FR3	TLYLOM I	TVFLEI TAFLRM	QFFLEI	raymgi
	GGGVVQPGF	GAEVRKPGT GGGLVQPGG	GPGL	GAEVI		FTISKDNSKNTLYI R	DRSSN' DNSKN'	DMSRS	NDDSTN'
임						RFTISE	RVSLTRDRSSNTVFL) RFTISRDNSKNTAFL)	RVSMS	RVTITA
SEQ ID	9 0 1 0	11	13	14	7	ರ[			
Name	A4 D2 D121	B2 D14	DS	A7	Name	CONT. 4 A4 D2 D121	B2 D14	D5	A7

#### FIG. 3B

<u>Name</u> A4 D2 D121 DP-46	SEQ ID NO: 8 9 10	FR1 GGGVVQPGRSLKLSCAASGFTFSAW.LRV	CDR1 SHGSH TM. .YTF.	FR2 WVRQAPGKGLEWVA	CDR2 LLSSDGSNKFYIESVKG TM. VI.YNK.Y.AD
B2 DP-7 D14 VH26	11 12	GAEVRKPGTSVRISCRASGNTFTKAKVKY GGGLVQPGGSLRLSCATSGFIFNAAAT.S	GHHIH SYYMH SYAMN	WVRQAPGQGLQWMG	RINPTGGGVSLAQSFQD ISST.YKG RISGNSGSTFYADSVKG ASGY
D5 IGHCAK	13	GPGLVRPSQTLSLTCPVSPGSIK	GDSYFWS SGY	WVRQPVGKGLEWIG .IA	RIYGRGTINYNRVFGS
A7 VH1-69	14	GAEVKKPGSSVKVSCRASGGTFS	RYAIS S	WVRQAPGQGLEWMG	GIIPPFGPVNYAQKFQG

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### FIG. 3B CONT'D

Name cont'd A4 D2 D121 DP-46	FR3  RFTISKDNSKNTLYLQMNSLRIDDTAVYYCAI RLSPETN RVER	CDR3 SLVGTTAFNY .EAD.	FR4 WGQGTLVTVSS	VH gene VH3 VH3
B2	RVSLTRDRSSNTVFLELSGLTEEDTALYFCAR	PRFNMIREPLDL	WGQGTVVTVSS	VH1
D14	RFTISRDNSKNTAFLRMNSQRAEDTAVYYCAK	DLSSGAYYYYGM DV	WGQGTTVTVSS	VH3
VH26	$\dots$			
DS IGHCAK	RVSMSVDMSRSQFFLELRDVTAADTAVYYCARTIT.KNS.K.SS	DKGSEYSYFDP	WGQGIVVNVFS	VH4
A7	RVTITADDSTNTAYMGLSSLRSGDTAVYYCAR	VAYDGSGYYNNI PKIYYYSYMDV	WGKGTTVTVSS	VH1
VH1-69	KSEE			

Clone	Closest	% amino acid	% nucleotide	R/S ratio	R/S ratio
	Germline	homology	homology	FRs	CDRs
A4	DP-46	98	68	6/6:1.0	12/5:2.4
D2	DP-46	87	92	8/6:1.3	4/5:0.8
D121	DP-46	91	95	2/4:0.5	7/0:>7.0
B2	DP-7	<i>L</i> 9	79	20/17:1.2	14/5:2.8
D14	VH26	87	93	7/3:2.3	5/2:2.5
D5	IGHCAK	73	81	17/16:1.1	13/4:3.3
A7	VH1-69	06	94	7/2:3.5	5/0:>5.0

#### FIG. 4A CDR's Heavy Chain

	CDR3	SLVGTTAFNY .EAD.	.t prfnmirepldl	DLSSGAYYYYGMDV	DKGSEYSYFDP	VAYDGSGYYNNIPKIYYYSYMDV	CDR3	QQYYDSYT QQLNSYPLT QQYGSSPRT	QQYYDSYT	QQYDNVPDT	QQYGTSPL	Hadasas
	Z ID		.i. PRF	910	DKC	VA3	<u>ain</u> SEQ ID NO:	50 51 52	53	54	55	ŭ
i	SEQ NO:		_		34	35	<b>CDR's Light Chain</b> CDR2	ES JOS AT	ES	'AT	.A.T	F
	CDR2	LLSSDGSNKFYIESVKG .IFYY.AD	vi.inn.i.ad Rinptgggvslaqsfqd	RISGNSGSTFYADSVKG	RIYGRGTTNYNRVFGS	GIIPPFGPVNYAQKFQG		WASTRES AASTLOS GASSRAT	WASTRES	GASSRAT	GASSRAT	FAGGGGG
	CD	LLSSDGSIFY	RINPIGG	RISGNSG	RIYGRGI	GIIPPFG	SEQ ID NO:	44 45	46	47	48	0
	SEQ ID NO:	222	25 25	26	27	28		INKNYLA 1 1A	SNNKNYLA	Ąī	Ą	Ę.
	CDR1	SHGSHTM.	. т.г	SYAMN	GDSYFWS	RYAIS	CDR1	KSSQSVFYTSNNKNYLA RASQGISSYLA RASQSVSSSYLA	KSSQSVFYTSN	RASQSVSSSYLA	RASQSVSSSYLA	PACOCYCCCVI.A
	SEQ ID	15 16	1.8	19	20	21	SEQ ID NO:	3 3 4 3 8 3 8	39	40	41	C

## Framework Regions, Heavy Chain

.EWVA	JOWMG JEWVS	EWIG	LEWMG	FR4 WGQGTLVTVSS WGQGTVVTVSS WGQGTTVTVSS	WGKGTTVTVSS
FR2 WVRQAPGKGLEWVA	WVRQAPGQGLQWMG WVRQAPGKGLEWVS	WVRQPVGKGLEWIG	WVRQAPGQGLEWMG	SEQ ID NO: 76 76 77 77	80
SEQ ID NO: 64 64 64	65 66	67	89		
FR1 GGGVVQPGRSLKLSCAASGFTFSAWLRV	GAEVRKPGTSVRISCRASGNTFT GGGLVQPGGSLRLSCATSGFIFN	GPGLVRPSQTLSLTCPVSPGSIK	GAEVKKPGSSVKVSCRASGGTFS	FR3  RFTISKDNSKNTLYLQMNSLRIDDTAVYYCAI RLSPETN RVSLTRDRSSNTVFLELSGLTEEDTALYFCAR RFTISRDNSKNTAFLRMNSQRAEDTAVYYCAR RVSMSVDMSRSQFFLELRDVTAADTAVYYCAR	RVTITADDSTNTAYMGLSSLRSGDTAVYYCAR
SEQ ID NO: 57 58 59	60 61	62	63	SEQ ID NO: 69 70 71 72 73	75

## FIG. 4B cont'd Framework Regions, Light Chain

SEQ ID NO:	FR1	SEQ ID NO:	FR2	
81 82 83	PDSLAVSLGERATINC PSFLSASVGDRVTITC PGTLSLSPGERATLSC	88 68 90	WYQQKPC WYQLKPC WYQQKPC	WYQQKPGQPPKLLIY WYQLKPGKAPKLLIY WYQQKPGQAPRLLIY
84	PDSLAVSLGERATINC	91	WYQQKPC	WYQQKPGQPPKLLIY
85	PGTLSLSPGEGATLSC	92	WYQQRPC	WYQQRPGQAPRLLIY
98	PGTLSLSPGEGATLSC	93	WYQQKP	WYQQKPGQAPRLLIY
87	PGTLSLSPGERVTLSC	94	WYQQKP	WYQQKPGQAPRLLIY
SEQ ID NO:	FR3	01	SEQ ID NO:	FR4
95 96 97	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC GVPSRFSGSGSGTEFTLTISSLQPEDFATYYC GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	Ö	102 103 104	FGQGTKLEIKRTVA FGGGAKVGIRRTVA FGQGTKVEIKRTVA
86	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC		105	FGQGTKLEIKRTVA
66	GIPDRESGSGSGTDFSFTISSLQPEDTGTYYC		106	FGQGTRLEIKRTVA
100	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC		107	FGQGTRLEIKRTVA
101	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC		108	FGQGTKVEIKRTVA

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FIG. 5A

# LIGHT CHAIN NUCLEOTIDE SEQUENCE OF ANTI-GPI ANTIBODIES

### A4 - SEQ ID NO:112

GAACTACTTAGCTTGGTACCAGCAGAAACCAGGCCAGCCTCCTAAGTTGCTCATTTACTGGGCATCCACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTAC TGTCAGCAATATTATGATTCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCT

### D2 - SEQ ID NO:113

CAGCTAAAACCGGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAG CCATCCTTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAAGGCATTAGCAGTTATTTAGCCTGGTAT TGGATCTGGGACAGAATTCACTCTCACAATAAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGCTTAATAGTT ACCCTCTCACTTTCGGCGGAGGGCCAAGGTGGGGATCAGACGAACTGTGGCT

### D121 – SEQ ID NO:114

GTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTG CCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTG GCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGT AG CTCACCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCT

### B2 - SEQ ID NO:115

GAACTACTTAGCTTGGTACCAGCAGAAACCAGGCCAGCCTCCTAAGTTGCTCATTTACTGGGCATCCACCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTAC CCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGGCCAGAGTGTTTTTACACTTCCAACAATAA TGTCAGCAATATTATGATTCGTACACTTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGAACTGTGGCT

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FIG. 5A cont'd

D14 – SEQ ID NO:116

GAAGTGGATCTGGGACAGATTTCAGTTTCACCATCAGCAGTCTGCAGCCTGAAGATACTGGGACATATTACTGTCAACAATATGAT AATGTCCCTGACACTTTTGGCCAGGGGACCAGGCTGGAGATCAAACGAACTGTGGCT

D5 - SEQ ID NO:117

GTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATGGTGCATCCAGTAGGGCCACTGGCATCCCAGACAGGTTCAGTG <u> CCAGGCACCCTGTCTTTGTCTCCAGGGGAAGGAGGACCACCCTCTCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCAGCTACTTAGCCTG</u> GCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGT ACCT CACCCCTCTTCGGCCAAGGGACACGACTGGAGATTAAACGAACTGTGGCT

A7 - SEQ ID NO:118

GTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTG GCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGACTTTGCAGTTTATTACTGTCAGCAGTATGGA AGCTCACCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCT

FIG. 5B

# HEAVY CHAIN NUCLEOTIDE SEQUENCE OF ANTI-GPI ANTIBODIES

A4-H - SEQ ID NO:116

GCCGATTCACCATCTCCAAGGACAATTCTAAGAACACACTGTATCTGCAAATGAACAGCCTGAGAATTGACGACACGGCTGTCTAT GAGGCGTGGTCCAGCCTGGGAGGTCCCTGAAACTCTCTGTGCAGCCTCTGGATTCACATTCAGTAGTCATGGCTCGCACTGGGTC CGCCAAGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACTTTTGTCGTCTGATGGAAGTAATAAATTCTATATAGAATCCGTGAAGG TACTGTGCGATTTCCCTGGTGGGAACTACCGCTTTTAACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

D2-H - SEQ ID NO:117

CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATTGAGCAGCCTAAGACCTGAGGACACGGCTGTCTATTA CCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACTTATATTCTATGATGGAAGTAATAATAATACTATGCAGACTCCGTGAAGGGC GGCGTGGTCCAAGCATGGAGGTCCCTAAGACTCTCCTGTGTAGCCTGTGGATTCACCTTCAGTAGTCATACCATGCACTGGGTCCG TTGTACGAATTCCGAGGTGGGAGCTACCGCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG

D121-H - SEQ ID NO:118

AGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACTCTATATCTGCAAATGAACAGCCTGAGAGTTGAGGACACGGCTGTT GGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTTTTCCTGTGCAGCCTCTGGATTCACCTTCAGTTCCTATACTTTCCACTGG GTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGCAGTTATATCATATGATGGAAACAAGAAATACTACGCAGACTCCGTGA 
 IATTACTGTGCGATTTCCATAGTGGGAACTACCGCTTTTAACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC

## where giving admits at the state of the stat

B2-H - SEQ ID NO:119

GGGGCTGAGGGTGAGGAAGCCCGGGACCTCCGTGAGGATCTCTTGCAGGGCATCTGGAAACACCTTCACTGGCACCATATTCACTG CAGGACAGAGTCAGCCTGACCAGGGACAGGTCGTCCAATACAGTCTTCTTGGAACTGAGCGGCCTCACGGAGGAGGACACGGCCT GGTCCGCCAGGCCCCTGGACAAGGCCTTCAGTGGATGGGAAGAATCAACCCGACTGGCGGCGGCGTTAGTCTCGCACAGAGTTTC TATATTTCTGTGCGAGGCCCCGATTTAACATGATCCGGGAACCTCTTGACCTCTGGGGGCCAGGGGACAGTGGTCACCGTCTCCTCA

D14-H - SEQ ID NO:120

AAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGGCGTTTCTGCGAATGAACAGCCAGAGAGCCGAAGACACGGCCG TITATTACTGTGCGAAAGATCTGTCGAGTGGTGCATACTACTACTACGGGATGGACGTCTGGGGCCAAGGGACCACGGTCACGTC GGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCTGTGCAACCTCTGGATTCATCTTTAACAGCTATGCCATGAACTG GGTCCGCCAGGCTCCAGGGAAGGGGCTTGAGTGGGTCTCACGTATTAGTGGAAATAGTGGAAGCACATTCTACGCAGACTCCGTG

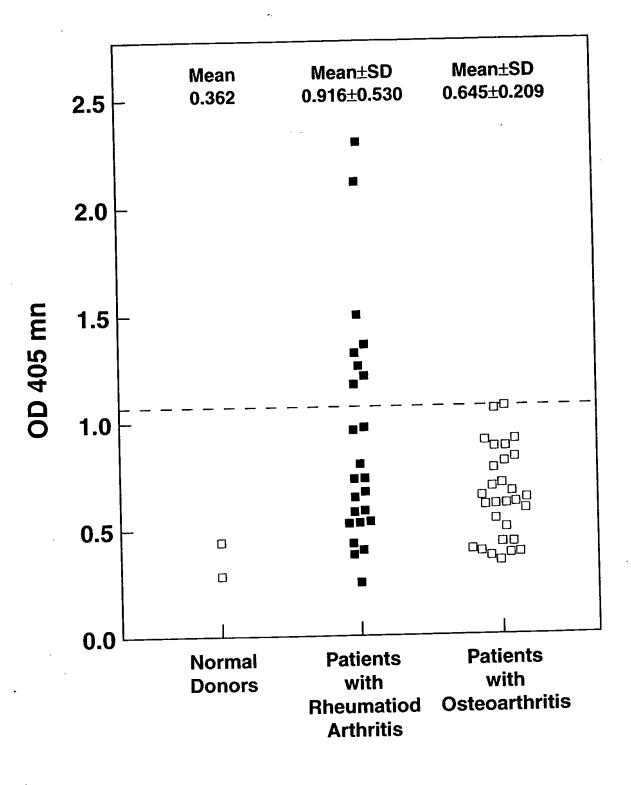
D5-H - SEQ ID NO:121

GGCCCAGGATTGGTGAGGCCATCACAGACCCTATCCCTCACCTGCACTGTCTCTCCAGGCTCCATTAAAAGGTGATAGTTACTTCTGG TCGGGAGTCGAGTCAGTATGTCAGTGGACATGTCCAGGAGTCAGTTTTTCTTGGAATTGAGAGATGTGACCGCCGCAGACACGGCC AGCTGGGTCCGTCAGCCCGTAGGGAAGGGACTGGAGTGGATAGGGCGTATCTACGGCAGAGGGACTACCAATTACAACCGTGTTT GTCTATTACTGTGCGAGAGACAAGGGGTCCGAATACTCCTACTTTGACCCCTGGGGGCCAGGGAATAGTGGTCAACGTCTTCTCA

### FIG. 5B CONT'D

A7-H - SEQ ID NO:122

ACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGATTCCACGAACACACAGCCTACATGGGTCTGAGCAGCC GGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAGGGCTTCTGGAGGCACATTCAGCAGATATGCTA TGAGATCTGGGGACACGGCCGTGTATTACTGCGCGAGAGTGGCCTATGATGGTAGTGGCTATTACAACAATATCCCAA AGATCTACTACTACTCCTACATGGACGTCTGGGGCAAAGGGACCACGGTCACCGTGTCCTCAGC



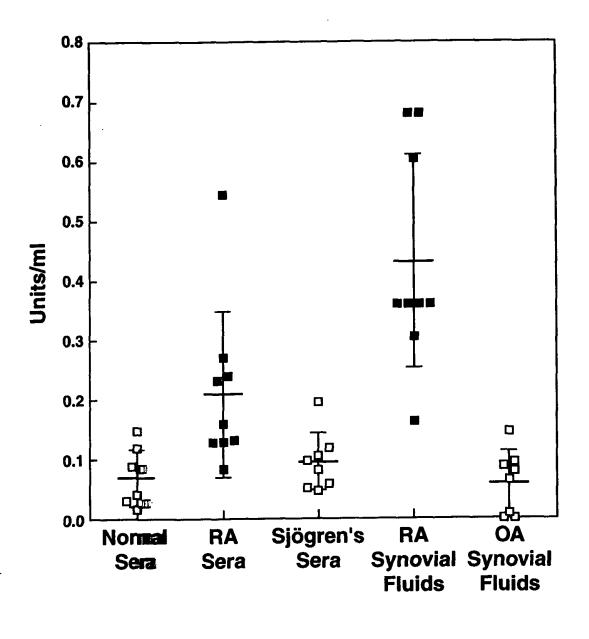
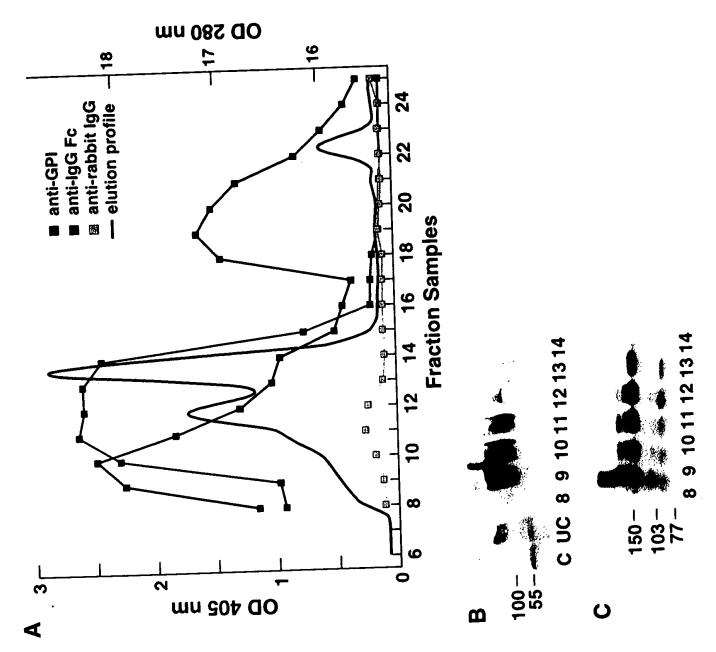
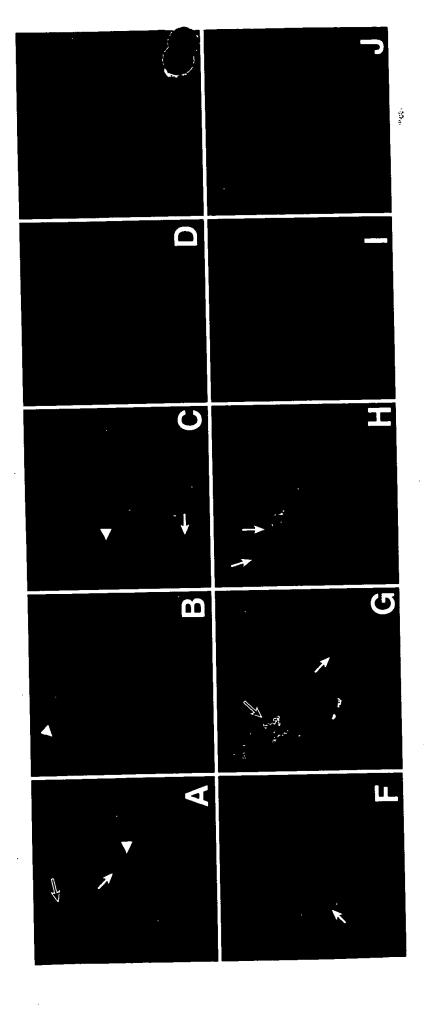


Fig. 7



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